



# Genetic characterization of *S. aureus* isolates from nasal carriage of healthy dairy goats

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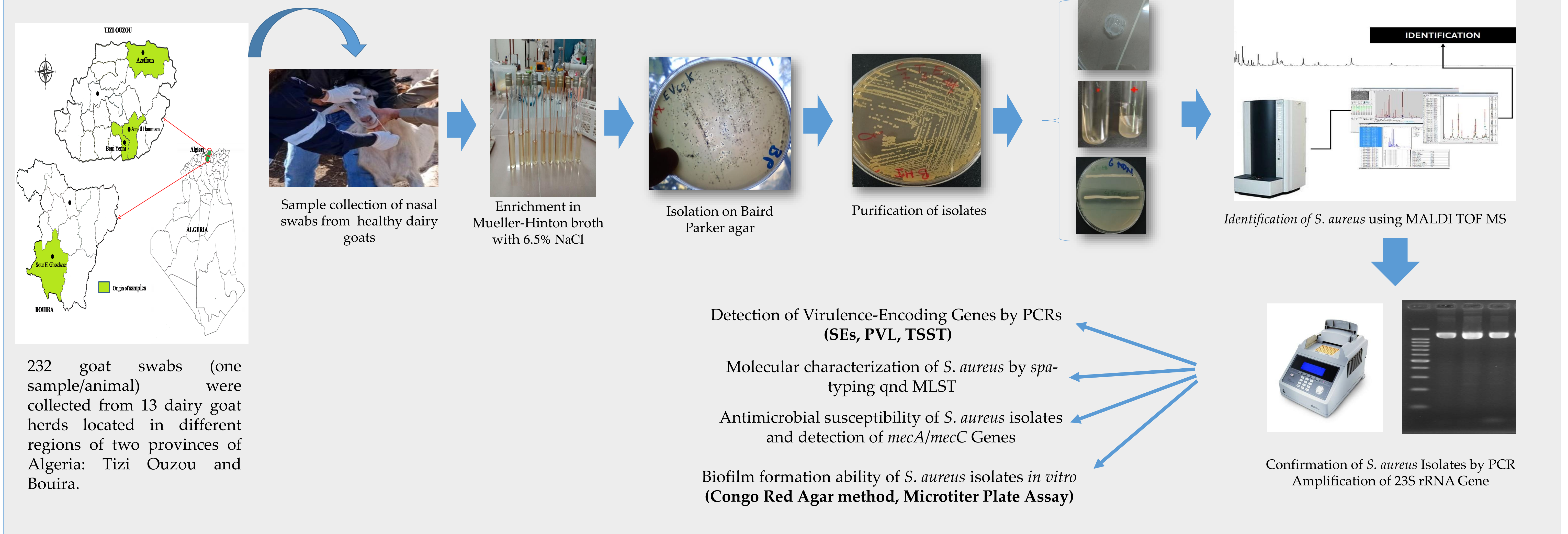
## 1. INTRODUCTION

Farm animals are a significant source of multidrug-resistant bacteria and antimicrobial-resistant genes. These bacteria include many zoonotic organisms that are frequently resistant to antibiotics, such as *Salmonella*, *Escherichia coli*, and *Staphylococcus aureus*, among others. In humans and many animal species, *Staphylococcus aureus* is considered to be a major opportunistic pathogen. In animals, it can cause a large array of diseases with considerable economic impacts in livestock animals. *S. aureus* colonizes its hosts without impacting their health, as is the case for any type of commensal bacterium. The most challenging characteristic of *S. aureus* that has become a global health concern is its capacity to acquire resistance against several antibiotic molecules, including methicillin. Methicillin-resistant *S. aureus* strains (MRSA) are a major global cause of infections in hospitals and communities. Recently, livestock-associated MRSA (LA-MRSA), mainly the complex clonal CC398, has been implicated in community infections.

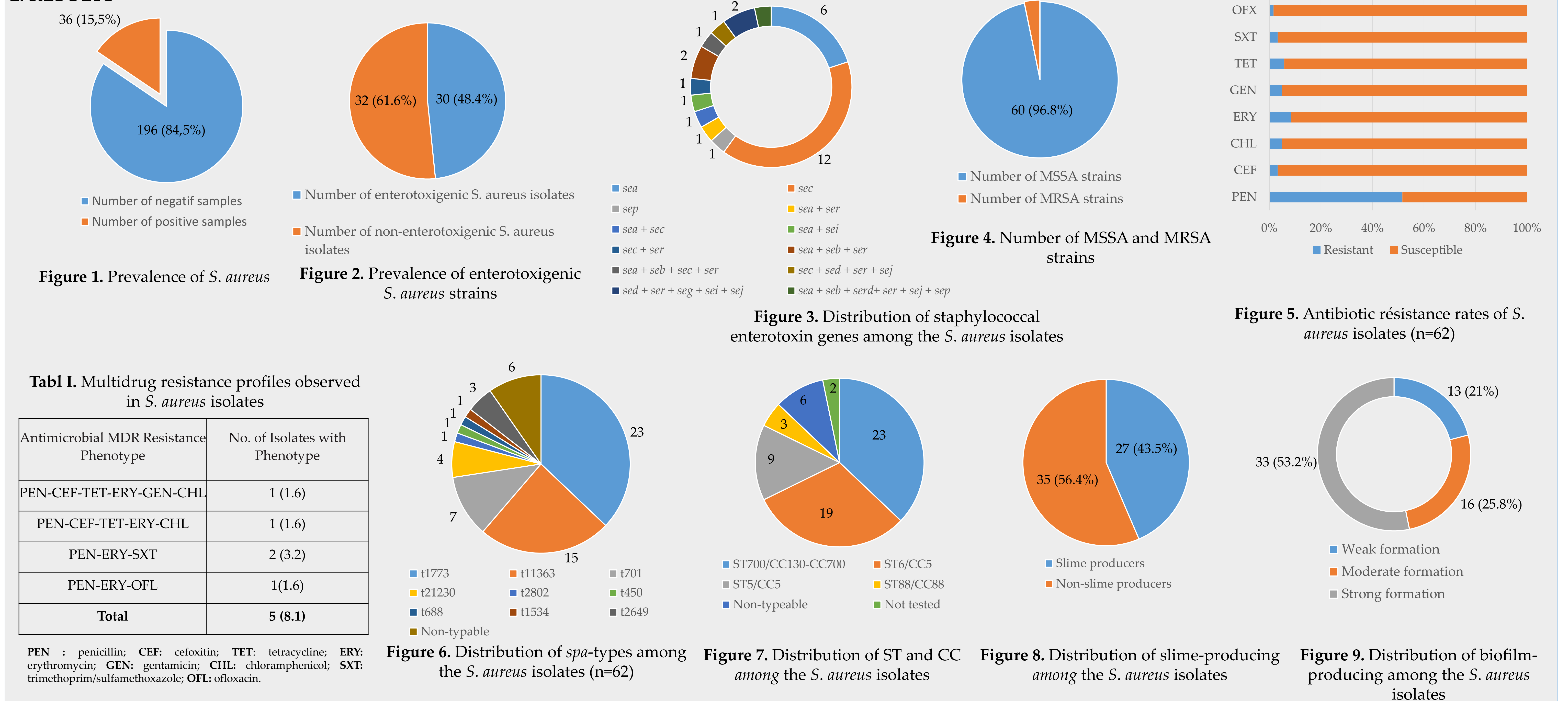
## Objectives of this study :

The aims of this study were to determine the prevalence of *S. aureus* in the nasal swabs of healthy dairy goats in two provinces of Algeria (Tizi Ouzou and Bouira) and to evaluate the phenotypic and genotypic characteristics of the recovered isolates.

## 2. MATERIALS AND METHODS



## 2. RESULTS



## 3. CONCLUSION

This study showed that the nares of healthy goats could be a reservoir of toxigenic and multidrug-resistant *S. aureus*. Clonal diversity in *S. aureus* isolates was observed, with a predominance of CC5. The presence of CC130/CC700 among our MSSA isolates is interesting, since the CC130 lineage is associated with *mecC* in the MRSA variant from human and animal isolates in Europe. Further expanded studies covering an extensive *S. aureus* population from different animal species collected in various geographical locations would give more information about the genetic lineages colonizing and infecting different livestock animals and their dissemination in the country.

